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Full Record**Details for HUGENEFL:U23752_AT****Full Screen**

NetAffx Links [Cluster Members](#)
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GeneChip Array Information

Probe Set ID U23752_at
**GeneChip
Array** HumanGeneFL Array
**Organism
Common
Name** Human

Probe Design Information

Transcript ID U23752
**Sequence
Type** Exemplar sequence
**Representative
Public ID** U23752 [NCBI](#)
**Target
Description** U23752, class A, 20 probes, 20 in U23752 1679-1919, Human SOX-11 mRNA, complete cds

Genomic Alignment of Target Sequence

Assembly April 2003 (NCBI 33)

	Position	% Identity	Cytoband
Alignment(s)	chr2: 5856192-5856457 (+) UCSC	99	p25.2

	Representative Transcript	UniGene Description	Position
Overlapping Transcripts	NM_003108 NCBI	SRY (sex determining region Y)- box 11	chr2:5854537-5863255 (+) UCSC

Public Domain and Genome References

Gene Title SRY (sex determining region Y)-box 11
Gene Symbol SOX11 [HGNC](#)
**Chromosomal
Location** 2p25
UniGene ID Hs.432638 [NCBI](#) (FULL LENGTH)
Ensembl ENSG00000176887 [Ensembl](#)
LocusLink 6664 [NCBI](#)
SwissProt P35716 [EMBL-EBI](#)
OMIM 600898 [NCBI](#)
**RefSeq Protein
ID** NP_003099 [NCBI](#)

RefSeq	RefSeq Transcript ID RefSeq Title			
	NM_003108 <u>NCBI</u> SRY-box 11			
Functional Annotations				
Ortholog	ID	Title	Organism	Type
	<u>RAE230A:1387275_AT</u>	SRY-box containing gene 11	Rat	Putative Ortholog
	<u>RG-U34A:AJ004858_AT</u>	SRY-box containing gene 11	Rat	Putative Ortholog
GO Biological Process (view graph)				
Gene Ontology	ID	Description	Evidence	Links
	6355	regulation of transcription, DNA-dependent	inferred from electronic annotation	QuickGO AmiGO
	7399	neurogenesis	traceable author statement	QuickGO AmiGO
	GO Cellular Component (view graph)			
	ID	Description	Evidence	Links
	5634	nucleus	inferred from electronic annotation	QuickGO AmiGO
	GO Molecular Function (view graph)			
	ID	Description	Evidence	Links
	3677	DNA binding	inferred from electronic annotation	QuickGO AmiGO
	Protein Similarities	Method	ID	Description
blast		4507161	SRY-box 11; SRY (sex-determining region Y)-box 11; SRY-related HMG-box gene 11; transcription factor SOX-11 [Homo sapiens]	0.0
blast		23831472		0.0
Protein Domains	Database	ID	Description	E-Value
	scop	<u>d1i11a_</u>	d1i11a_ SCOP:a.21.1.1: Sox-5	2.36E-19
	pfam	<u>HMG_box</u>	HMG (high mobility group) box	1.1E-33
	InterPro	IPR000910	HMG1/2 (high mobility group) box	
		EMBL-EBI		

Sequence

>HUGENEFL:U23752_AT
 cttcctttatcgtgtctcaaggtagttgcatacctagtcctggagttgtgattatatttccc
 aaaaaatgtgtttttgtaattactattttcttttctgaaattcgtgattgcaacaaagg
 cagagggggcggcgcgcgaggaggtaggaccgcgtccggaaggcgctgtttgaagc
 ttgtcggctctttgaagtcctggaagacgtctgcagaggacccttttggcagcacaactgtt
 actctagggagttggtggagatatt

Target Sequence

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
CTTCCTTTATCGTGTCTCAAGGTAG	503	219	1691	Antisense
TTATCGTGTCTCAAGGTAGTTGCAT	504	219	1697	Antisense
TCGTGTCTCAAGGTAGTTGCATACC	505	219	1700	Antisense
AAGGTAGTTGCATACCTAGTCTGGA	506	219	1709	Antisense
GTAGTTGCATACCTAGTCTGGAGTT	507	219	1712	Antisense

Probe Info	GTTGCATACCTAGTCTGGAGTTGTG	508	219	1715	Antisense
	TACCTAGTCTGGAGTTGTGATTATT	509	219	1721	Antisense
	CTAGTCTGGAGTTGTGATTATTTTC	510	219	1724	Antisense
	TGTGATTATTTTCCCAAAAATGTG	511	219	1736	Antisense
	TTTTCCTGAAATTCGTGATTGCAAC	512	219	1781	Antisense
	GCTCCGGAAGGCGCTGTTTGAAGCT	513	219	1847	Antisense
	GCTGTTTGAAGCTTGTCGGTCTTTG	514	219	1859	Antisense
	TGAAGCTTGTCGGTCTTTGAAGTCT	515	219	1865	Antisense
	TTGTCGGTCTTTGAAGTCTGGAAGA	516	219	1871	Antisense
	TGGAAGACGTCTGCAGAGGACCCTT	517	219	1889	Antisense
	AAGACGTCTGCAGAGGACCCTTTTG	518	219	1892	Antisense
	GCAGAGGACCCTTTTGGCAGCACAA	519	219	1901	Antisense
	AGCACAACTGTTACTCTAGGGAGTT	520	219	1919	Antisense
	ACTGTTACTCTAGGGAGTTGGTGA	521	219	1925	Antisense
	ACTCTAGGGAGTTGGTGGAGATATT	522	219	1931	Antisense

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